

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 20:28:47 ; Search time 2320 Seconds
(without alignments)
9189.782 Million cell updates/sec

Title: US-09-976-054-5

Perfect score: 440
Sequence: 1 cgtccgcgcgcgcgcgcacattc.....ggaatnctagataaaaaant 440

Scoring table:
IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank1:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	28.4	993	8 AK104808	AK104808 Oryza sat
2	125	28.4	1001	8 AK104107	AK104107 Oryza sat
3	125	28.4	1010	8 AK073627	AK073627 Oryza sat
4	123.6	28.1	975	8 AB012046	AB012046 Hordeum v
5	123.2	28.0	845	8 TA022442	TA022442 Triticum ae
6	107.8	24.5	204120	8 AY61659	AY61659 Sorghum b
7	93	21.1	848	8 AY324112	AY324112 Brassica
8	92.8	21.1	279	6 AR247242	AR247242 Sequence
9	91.4	20.8	893	8 BT012816	BT012816 Lycopersi
10	86.4	20.1	1036	8 AY084300	AY084300 Arabidops
11	86.6	19.7	729	8 ATNAPT	ATNAPT Arabidops
12	86.6	19.7	811	8 BT000370	BT000370 Arabidops
13	86.6	19.7	879	8 AF325045	AF325045 Arabidops
14	86.6	19.7	887	8 AY128377	AY128377 Arabidops
15	80.2	18.2	806	8 AK108481	AK108481 Oryza sat
16	80.2	18.2	1122	8 AY338894	AY338894 Oryza sat
17	80.2	18.2	1354	8 AK121982	AK121982 Oryza sat
18	77.6	17.6	1202	8 AY485263	AY485263 Zea mays
19	77	17.5	552	6 C0805734	C0805734 Sequence

20	77	17.5	583	8 BT004412	BT004412 Arabidops
21	77	17.5	846	8 BT002969	BT002969 Arabidops
22	77	17.5	847	8 AY084513	AY084513 Arabidops
23	76.6	17.4	1097	8 AY255503	AY255503 Triticum
24	73	16.6	1038	8 AK070784	AK070784 Oryza sat
25	73	16.6	1065	8 AK069606	AK069606 Oryza sat
26	72.4	16.5	579	8 AY133689	AY133689 Arabidops
27	72.4	16.5	700	8 BT001111	BT001111 Arabidops
28	69	15.7	579	8 BT001122	BT001122 Arabidops
29	69	15.7	727	8 ATNPT2	ATNPT2 Arabidops
30	69	15.7	850	8 AT072021	AT072021 Arabidops
31	67	15.2	607	8 BT005077	BT005077 Arabidops
32	67	15.2	995	8 BT004028	BT004028 Arabidops
33	58.4	13.3	110000	1 AE017282_08	Continuation (9 of
34	58	13.2	143895	8 CNE08CD6	AE017282_08
35	52.2	11.9	106702	8 ATPTK2	ATPTK2 Oryza sat
36	52.2	11.9	199577	8 ATCHRIV57	ATCHRIV57 Arabidops
37	52	11.8	297850	1 AP006577	AP006577 Gloeobact
38	51.8	11.8	346259	1 BX640435	BX640435 Bordetell
39	51.8	11.8	346287	1 BX640450	BX640450 Bordetell
40	51.2	11.6	86209	8 CNE04523	CNE04523 Lotus cor
41	51.2	11.6	132741	8 CNE08CMA	CNE08CMA Oryza sat
42	50.2	11.4	10172	1 AE004187	AE004187 Oryza sat
43	50.2	11.4	346359	1 BX640411	BX640411 Bordetell
44	49.8	11.3	13614	1 AE006072	AE006072 Pasteurel
45	49.8	11.3	190050	1 AL646059	AL646059 Ralstonia

ALIGNMENTS

RESULT 1
AK104808
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:001-040-B09, full
insert sequence.
ACCESSION
AK104808
VERSION
AK104808.1 GI:32990017
KEYWORDS
FLI CDNA; oligo capping.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Rhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

1 The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team;
Kikuchi, S., Sato, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, B., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Oono, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mura, J.,
Kusunagi, T., Oka, M., Ryu, R., Ueda, M., Matsumura, K., RIKEN;
Kawa, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Ogasato, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)

TITLE

JOURNAL
MEDLINE
22752273
Science 301 (5631), 376-379 (2003)

REFERENCE

PUBMED

2 (bases 1 to 993)

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,

*Alignment of SEQ/DNA.5
to wheat sequence*

RESULT 5
TAU22442
LOCUS
DEFINITION Triticum aestivum adenine phosphoribosyltransferase form 1 (APT1)
ACCESSION U22442
VERSION U22442.1 GI:726304
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 845)
Moffatt,B.A., Schnorr,K., Galliard,C., Biget,E. and Laloue,M.
Nucleotide sequence of a wheat cDNA encoding Adenine
Phosphoribosyltransferase (Genbank U22442) (PGR95-030)
Plant Physiol. 108 (4), 1748 (1995)
2 (bases 1 to 845)
Schnorr,K.S., Moffatt,B.A., Biget,E. and Laloue,M.
Direct Submision
Submitted (10-MAR-1995) Kirk Matthew Schnorr, Department of
Biological Chemistry, Institute of Molecular Biology, University of
Copenhagen, Solvgade 83, Copenhagen K, DK 1307, Denmark
Location/Qualifiers
1..845
/organism="Triticum aestivum"
/mol_type="mRNA"
/strain="Capitol"
/db_xref="taxon:4565"
/tissue_type="Immature seeds"
/dev_stage="23 days after flowering"
1..845
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/gene="APT1"
/gene="APT1"
/gene="APT1"
/EC_number="2.4.2.7"
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/note="APRT"
/codon_start=1
/product="adenine phosphoribosyltransferase form 1"
/protein_id="AAA0609.1"
/db_xref="GI:726305"
/translation="MADGKVERIASIRAIINPKPKGILFQDITLLDPOAFRTT
DLFERYKDDITVAVGKARGFIPPIALAGAKVPIKPKDLPKAVISEYSLD
YGTDKEMHVGAVQPNRVLIIVDLIANGTLCAAKLIRVGAKEACVIELPEL
KGRDKADMVPTVQADESV"
594..845
/gene="APT1"
/gene="APT1"
/note="20 A nucleotides"
ORIGIN
3' UTR
polyA_site
CDS
5' UTR
gene
FEATURES
source

Query Match 28.0%; Score 123.2; DB 8; Length 845;
Best Local Similarity 66.1%; Pred. No. 2.2e-18;
Matches 211; Conservative 0; Mismatches 101; Indels 7; Gaps 4;

QY	77	GCAGGCGAGGCGAGCGGCTGTGCGATGGCGTNCCTGATGCCGCTTGGCGGAGATCG	136
DB	22	GGGGGCGAGGCTCGGCGGCGGCTGTGCGATGCC--GAAGGCGGCGGTGAGCGGATCG	78
QY	137	NTCCCTNATCNGGWTATNCCGACTNCCAAAGCCAGGATNATGTTTCAGACATCA	196
DB	79	CGTCAGATTCGGCCATCCCACTTCCCAAGCCAGGATTTTGTTCAGACATCA	138
QY	197	NGANGTNTGTTGATCCCAAGCGGNTCCGTGACACATATACATTTTGTCAAGCGGT	256
DB	139	CAACTTCTCTGTGATTCGAGGATTCGGTGACACATGACCTCTTGTGAGCGGT	198
QY	257	ACAAGACCAAGGATCAACNTGAAANTAGAGATTAAAGCTAGAGGATCANTTTCGA	316
DB	199	ACAAGACCAAGACATTAAGTGTGCT-GGTGTGAAGCCAGAGGATTCATTTTGT	257
QY	317	ACAATANNCTTAAANNAATTGTCAAAATNGTGCNATGAGGAGGNNATNAG	376
DB	258	CCTCCATTGC--ATTAGCCATTAGGTGCAAGTTGT--TCCATTAAGGAGGCCGAAAAA	314
QY	377	NTGCCANGCNAATGATTT	395
DB	315	TTACTCTGTGAGGTGATAT	333

